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SEQUENCE LISTING

<110> Mack, David
Gish, Kurt
EOS Biotechnology, Inc.

<120> Methods of Diagnosis of Breast Cancer, Compositions and Methods of Screening for Modulators of Breast Cancer

<130> 018501-001200US

<140> US 09/829,472
<141> 2001-04-09

<150> US 09/525,361
<151> 2000-03-15

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<170> PatentIn Ver. 2.1

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Lys Leu Pro Cys Phe Tyr Arg Gly Asp Ser Gly Glu Gln Val Gly Gln
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Val Ala Trp Ala Arg Val Asp Ala Gly Glu Gly Ala Gln Glu Leu Ala
 65                  70                  75                  80

Leu Leu His Ser Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Gly
                 85                  90                  95

Arg Val Glu Gln Pro Pro Pro Pro Arg Asn Pro Leu Asp Gly Ser Val
            100                 105                 110

Leu Leu Arg Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg
        115                 120                 125

Val Ser Thr Phe Pro Ala Gly Ser Phe Gln Ala Arg Leu Arg Leu Arg
    130                 135                 140

Val Met Val Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Ala Leu Glu
145                 150                 155                 160

Glu Gly Gln Gly Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser
                165                 170                 175

Pro Ala Pro Ser Val Thr Trp Asp Thr Glu Val Lys Gly Thr Thr Ser
            180                 185                 190

Ser Arg Ser Phe Lys His Ser Arg Ser Ala Ala Val Thr Ser Glu Phe
        195                 200                 205

His Leu Val Pro Ser Arg Ser Met Asn Gly Gln Pro Leu Thr Cys Val
    210                 215                 220

Val Ser His Pro Gly Leu Leu Gln Asp Gln Arg Ile Thr His Ile Leu
225                 230                 235                 240

His Val Ser Phe Leu Ala Glu Ala Ser Val Arg Gly Leu Glu Asp Gln
                245                 250                 255

Asn Leu Trp His Ile Gly Arg Glu Gly Ala Met Leu Lys Cys Leu Ser
            260                 265                 270

Glu Gly Gln Pro Pro Pro Ser Tyr Asn Trp Thr Arg Leu Asp Gly Pro
        275                 280                 285

Leu Pro Ser Gly Val Arg Val Asp Gly Asp Thr Leu Gly Phe Pro Pro
    290                 295                 300

Leu Thr Thr Glu His Ser Gly Ile Tyr Val Cys His Val Ser Asn Glu
305                 310                 315                 320
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Phe Ser Ser Arg Asp Ser Gln Val Thr Val Asp Val Leu Asp Pro Gln
                325                 330                 335

Glu Asp Ser Gly Lys Gln Val Asp Leu Val Ser Ala Ser Val Val Val
            340                 345                 350

Val Gly Val Ile Ala Ala Leu Leu Phe Cys Leu Leu Val Val Val Val
        355                 360                 365

Val Leu Met Ser Arg Tyr His Arg Arg Lys Ala Gln Gln Met Thr Gln
    370                 375                 380

Lys Tyr Glu Glu Glu Leu Thr Leu Thr Arg Glu Asn Ser Ile Arg Arg
385                 390                 395                 400

Leu His Ser His His Thr Asp Pro Arg Ser Gln Pro Glu Glu Ser Val
                405                 410                 415

Gly Leu Arg Ala Glu Gly His Pro Asp Ser Leu Lys Asp Asn Ser Ser
            420                 425                 430

Cys Ser Val Met Ser Glu Glu Pro Glu Gly Arg Ser Tyr Ser Thr Leu
        435                 440                 445

Thr Thr Val Arg Glu Ile Glu Thr Gln Thr Glu Leu Leu Ser Pro Gly
    450                 455                 460

Ser Gly Arg Ala Glu Glu Glu Glu Asp Gln Asp Glu Gly Ile Lys Gln
465                 470                 475                 480

Ala Met Asn His Phe Val Gln Glu Asn Gly Thr Leu Arg Ala Lys Pro
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Thr Gly Asn Gly Ile Tyr Ile Asn Gly Arg Gly His Leu Val
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<222> (1)..(486)
<223> Xaa = any amino acid

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             20                  25                  30

Leu Glu Thr Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala Lys
         35                  40                  45
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```
Leu Pro Cys Phe Tyr Arg Gly Asp Pro Asp Glu Gln Val Gly Gln Val
     50                  55                  60

Ala Trp Ala Arg Val Asp Pro Asn Glu Xaa Tyr Pro Gly Ala Gly Leu
 65                  70                  75                  80

Leu His Ser Lys Tyr Gly Leu His Val Asn Pro Ala Tyr Glu Asp Arg
                 85                  90                  95

Val Glu Gln Xaa Xaa His Glu Thr Phe Arg Arg Ser Val Leu Leu Arg
            100                 105                 110

Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg Val Ser Thr
        115                 120                 125

Phe Pro Ser Gly Ser Phe Gln Ala Arg Met Arg Leu Arg Val Leu Val
    130                 135                 140

Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Pro Leu Glu Glu Gly Gln
145                 150                 155                 160

Ala Asp Val Ala Ala Ser Cys Thr Ala Glu Gly Ser Pro Ala Pro Ser
                165                 170                 175

Val Thr Trp Asp Thr Glu Val Lys Gly Thr Gln Ser Ser Arg Ser Phe
            180                 185                 190

Thr His Pro Arg Ser Ala Ala Val Thr Ser Glu Phe His Leu Val Pro
        195                 200                 205

Ser Arg Ser Met Asn Gly Gln Pro Leu Thr Cys Val Val Ser His Pro
    210                 215                 220

Gly Leu Leu Gln Asp Arg Arg Ile Thr His Thr Leu Gln Val Ala Phe
225                 230                 235                 240

Leu Ala Glu Ala Ser Val Arg Gly Leu Glu Asp Gln Asn Leu Trp Gln
                245                 250                 255

Val Gly Arg Glu Gly Ala Thr Leu Lys Cys Leu Ser Glu Gly Gln Pro
            260                 265                 270

Pro Pro Lys Tyr Asn Trp Thr Arg Leu Asp Gly Pro Leu Pro Ser Gly
        275                 280                 285

Val Arg Val Lys Gly Asp Thr Leu Gly Phe Pro Pro Leu Thr Thr Glu
    290                 295                 300

His Ser Gly Val Tyr Xaa Cys His Val Ser Asn Glu Leu Ser Ser Arg
305                 310                 315                 320

Asp Ser Gln Val Thr Val Glu Val Leu Asp Pro Glu Asp Pro Gly Lys
                325                 330                 335

Gln Val Asp Leu Val Ser Ala Ser Val Ile Ile Val Gly Val Ile Ala
            340                 345                 350

Ala Leu Leu Phe Cys Leu Leu Val Val Val Val Val Leu Met Ser Arg
        355                 360                 365
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Tyr His Arg Arg Lys Ala Gln Gln Met Thr Gln Lys Tyr Glu Glu Glu
    370                 375                 380

Leu Thr Leu Thr Arg Glu Asn Ser Ile Arg Arg Leu His Ser His His
385                 390                 395                 400

Ser Asp Pro Arg Ser Gln Pro Glu Glu Ser Val Gly Leu Arg Ala Glu
                405                 410                 415

Gly His Pro Asp Ser Leu Lys Asp Asn Ser Ser Cys Ser Val Met Ser
            420                 425                 430

Glu Glu Pro Glu Gly Arg Ser Tyr Ser Thr Leu Thr Thr Val Arg Glu
        435                 440                 445

Ile Glu Thr Gln Thr Glu Leu Leu Ser Pro Gly Ser Gly Arg Thr Glu
    450                 455                 460

Glu Asp Asp Asp Gln Asp Glu Gly Ile Lys Gln Ala Met Asn His Leu
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Cys Arg Lys Met Gly Pro
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<220>
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<400> 9

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             20                  25                  30

Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
         35                  40                  45

Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
     50                  55                  60

Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
 65                  70                  75                  80
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Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
                 85                  90                  95

Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
            100                 105                 110

Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
        115                 120                 125

Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
    130                 135                 140

Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145                 150                 155                 160

Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
                165                 170                 175

Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
            180                 185                 190

Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
        195                 200                 205

Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
    210                 215                 220

Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
225                 230                 235                 240

Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
                245                 250                 255

Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
            260                 265                 270

Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
        275                 280                 285

Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
    290                 295                 300

Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
305                 310                 315                 320

Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
                325                 330                 335

Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys
            340                 345                 350

Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
        355                 360                 365

Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala
    370                 375                 380

Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu
385                 390                 395                 400
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Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile
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Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
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Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
435 440 445

Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
450 455 460

Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
465 470 475 480

Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val
485 490 495

Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
500 505 510

Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
515 520 525

Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
530 535 540

Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
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Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
565 570 575

Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
580 585 590

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Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly Val Leu Phe Cys
625 630 635 640

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645 650 655

Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro His Thr Pro Pro
660 665 670

Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser Asp Gly Asn Phe
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770 775 780

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820 825 830

Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp Phe Val Arg Leu
835 840 845

Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys Gly Ser Gly Gln
850 855 860

Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala Phe Gly Pro Gly
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Thr Ala Thr Gln Thr Leu Met Thr Met Tyr Arg Arg Arg Ser Pro Glu
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Glu Lys Thr Arg Glu Leu Val Leu Lys Gly Ile Pro Glu Ser Met Arg
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Gly Glu Leu Trp Leu Leu Leu Ser Gly Ala Ile Asn Glu Lys Ala Thr
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His Pro Gly Tyr Tyr Glu Asp Leu Val Glu Lys Ser Met Gly Lys Tyr
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Asn Leu Ala Thr Glu Glu Ile Glu Arg Asp Leu His Arg Ser Leu Pro
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Glu His Pro Ala Phe Gln Asn Glu Met Gly Ile Ala Ala Leu Arg Arg
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Val Leu Thr Ala Tyr Ala Phe Arg Asn Pro Asn Ile Gly Tyr Cys Gln
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Ala Met Thr Val Leu Gly Arg Tyr Leu Asp Ser Val Thr Asn Lys Asp
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Ser Thr Leu Pro Pro Ile Pro His Leu His Ser Leu Leu Ser Asp Asp
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Arg Asn Val Val Arg Thr Ile Val Thr Glu Thr Ser Phe Thr Ile Asp
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Cys Tyr Trp Gly Gly Ser Ser Asn Ala Leu Asp Arg His Asp Pro Ser
465                 470                 475                 480

Leu Pro Tyr Leu Glu Gln Tyr Arg Ile Asp Phe Glu Gln Phe Lys Gly
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Asp Leu Thr Glu Lys Leu Lys Leu Leu Tyr Lys Met His Val Leu Pro
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Asn Tyr Leu Arg Leu Trp Thr Pro Glu Asn Lys Ser Lys Ser Lys Asn
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Ala Lys Asp Leu Pro Lys Leu Asn Gln Gly Gln Phe Ile Glu Leu Cys
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Lys Thr Met Tyr Asn Met Phe Ser Glu Asp Pro Asn Glu Gln Glu Leu
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Tyr His Ala Thr Ala Ala Val Thr Ser Leu Leu Leu Glu Ile Gly Glu
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Val Gly Lys Leu Phe Val Ala Gln Pro Ala Lys Glu Gly Gly Ser Gly
690 695 700

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Lys Lys Gly Pro Gly Gln Pro Tyr Val Val Glu Ser Val Glu Pro Leu
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Met Glu Asp Ile Lys Leu Glu Asp Ser Ser Pro Arg Asp Asn Gly Ala
755 760 765

Cys Ser Ser Met Leu Ile Ser Asp Asp Asp Thr Lys Asp Asp Ser Ser
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Met Ser Ser Tyr Ser Val Leu Ser Ala Gly Ser His Glu Glu Asp Lys
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Gln Gly Thr Ala Ala Leu Pro Arg Ser Thr Ser Leu Asp Arg Asp Trp
820 825 830

Ala Ile Thr Phe Glu Gln Phe Leu Ala Ser Leu Leu Thr Glu Pro Ala
835 840 845

Leu Val Lys Tyr Phe Asp Lys Pro Val Cys Met Met Ala Arg Ile Thr
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His Gly Val Ile Thr Glu Asn Asn Asp Thr Val Ile Leu Asp Pro Pro
     50                  55                  60

Leu Val Ala Leu Asp Lys Asp Ala Pro Val Pro Phe Ala Gly Glu Ile
 65                  70                  75                  80

Cys Ala Phe Lys Ile His Gly Gln Glu Leu Pro Phe Glu Ala Val Val
                 85                  90                  95

Leu Asn Lys Thr Ser Gly Glu Gly Arg Leu Arg Ala Lys Ser Pro Ile
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Asp Cys Glu Leu Gln Lys Glu Tyr Thr Phe Ile Ile Gln Ala Tyr Asp
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Lys Pro Ala Ala Gln Asp Thr Leu Val Gln Val Asp Val Lys Pro Val
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Cys Lys Pro Gly Trp Gln Asp Trp Thr Lys Arg Ile Glu Tyr Gln Pro
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Gln Ala Asp Thr Phe Arg Pro Ala Glu Phe His Trp Lys Leu Asp Gln
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Val Gly Ala Cys Trp Gln Gly Gly Glu Val Thr Lys Pro Gln Phe Ala
            500                 505                 510

Gln Phe Phe His Gly Ser Leu Ala Ser Leu Thr Ile Arg Pro Gly Lys
        515                 520                 525

Met Glu Ser Gln Lys Val Ile Ser Cys Leu Gln Ala Cys Lys Glu Gly
    530                 535                 540

Leu Asp Ile Asn Ser Leu Glu Ser Leu Gly Gln Gly Ile Lys Tyr His
545                 550                 555                 560

Phe Asn Pro Ser Gln Ser Ile Leu Val Met Glu Gly Asp Asp Ile Gly
                565                 570                 575

Asn Ile Asn Arg Ala Leu Gln Lys Val Ser Tyr Ile Asn Ser Arg Gln
            580                 585                 590

Phe Pro Thr Ala Gly Val Arg Arg Leu Lys Val Ser Ser Lys Val Gln
        595                 600                 605

Cys Phe Gly Glu Asp Val Cys Ile Ser Ile Pro Glu Val Asp Ala Tyr
    610                 615                 620

Val Met Val Leu Gln Ala Ile Glu Pro Arg Ile Thr Leu Arg Gly Thr
625                 630                 635                 640

Asp His Phe Trp Arg Pro Ala Ala Gln Phe Glu Ser Ala Arg Gly Val
                645                 650                 655

Thr Leu Phe Pro Asp Ile Lys Ile Val Ser Thr Phe Ala Lys Thr Glu
            660                 665                 670

Ala Pro Gly Asp Val Lys Thr Thr Asp Pro Lys Ser Glu Val Leu Glu
        675                 680                 685

Glu Met Leu His Asn Leu Asp Phe Cys Asp Ile Leu Val Ile Gly Gly
    690                 695                 700

Asp Leu Asp Pro Arg Gln Glu Cys Leu Glu Leu Asn His Ser Glu Leu
705                 710                 715                 720

His Gln Arg His Leu Asp Ala Thr Asn Ser Thr Ala Gly Tyr Ser Ile
                725                 730                 735

Tyr Gly Val Gly Ser Met Ser Arg Tyr Glu Gln Val Leu His His Ile
            740                 745                 750

Arg Tyr Arg Asn Trp Arg Pro Ala Ser Leu Glu Ala Arg Arg Phe Arg
        755                 760                 765
```

```
Ile Lys Cys Ser Glu Leu Asn Gly Arg Tyr Thr Ser Asn Glu Phe Asn
    770                 775                 780

Leu Glu Val Ser Ile Leu His Glu Asp Gln Val Ser Asp Lys Glu His
785                 790                 795                 800

Val Asn His Leu Ile Val Gln Pro Pro Phe Leu Gln Ser Val His His
                805                 810                 815

Pro Glu Ser Arg Ser Ser Ile Gln His Ser Ser Val Val Pro Ser Ile
            820                 825                 830

Ala Thr Val Val Ile Ile Ile Ser Val Cys Met Leu Val Phe Val Val
        835                 840                 845

Ala Met Gly Val Tyr Arg Val Arg Ile Ala His Gln His Phe Ile Gln
    850                 855                 860

Glu Thr Glu Ala Ala Lys Glu Ser Glu Met Asp Trp Asp Asp Ser Ala
865                 870                 875                 880

Leu Thr Ile Thr Val Asn Pro Met Glu Lys His Glu Gly Pro Gly His
                885                 890                 895

Gly Glu Asp Glu Thr Glu Gly Glu Glu Glu Glu Glu Ala Glu Glu Glu
            900                 905                 910

Met Ser Ser Ser Ser Gly Ser Asp Asp Ser Glu Glu Glu Glu Glu Glu
        915                 920                 925

Glu Gly Met Gly Arg Gly Arg His Gly Gln Asn Gly Ala Arg Gln Ala
    930                 935                 940

Gln Leu Glu Trp Asp Asp Ser Thr Leu Pro Tyr
945                 950                 955
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<210> 16
<211> 2616
<212> DNA
<213> Homo sapiens

<220>
<223> BFG7, EST, type III membrane protein

<220>
<221> CDS
<222> (1)..(906)
<223> BFG7

<400> 16
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gactgcgtac tgcagtgcga agagcagaac tgctctgggg gcgctctgaa tcacttccgc 180
tcccgccagc caatctacat gagtctagca ggctggacct gtcgggacga ctgtaagtat 240
gagtgtatgt gggtcaccgt tgggctctac ctccaggaag gtcacaaagt gcctcagttc 300
catggcaagt ggcccttctc ccggttcctg ttctttcaag agccggcatc ggccgtggcc 360
tcgtttctca atggcctggc cagcctggtg atgctctgcc gctaccgcac cttcgtgcca 420
gcctcctccc ccatgtacca cacctgtgtg gccttcgcct gggtgtccct caatgcatgg 480
ttctggtcca cagtyttcca caccagggac actgacctca cagagaaaat ggactacttc 540
tgtgcctcca ctgtcatcct acactcaatc tacctgtgct gcgtcagcct catccgcttc 600

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gactatggct acaacctggt ggccaacgtg gctattggcc tggtcaacgt ggtgtggtgg 660
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gtcttgctgc tgcaggggct gtccctgctc gagctgcttg acttcccacc gctcttctgg 780
gtcctggatg cccatgccat ctggcacatc agcaccatcc ctgtccacgt cctcttttc 840
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gccgtgagca tgggcctggg tgtgtgtgag ctcaggcact aggtgcgcag tgtggagacg 1680
ggtgttgtcg gggaagaggt gtggcttcaa agtgttgtgt gtgcaggggg tkggtgtgtt 1740
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ctggccttcc cctccaaaac ctccattccc ctgctgccag ccccttgcc atagcctgat 2160
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gaggggagct atgctaggac tccaacctca gggactcggg tggcctgcgc tagcttcttt 2520
tgatactgaa aacttttaag gtgggagggt ggcaagggat gtgcttaata aatcaattcc 2580
aagcctcaaa aaaaaaaaaa aaaaaaaaaa aaaaaa                          2616
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<210> 17
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<223> BFG7, EST, type III membrane protein

<400> 17

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Arg Val Asp Pro Arg Val Arg Gly Glu Arg Met Ala Gly Leu Ala Ala
  1               5                  10                  15

Arg Leu Val Leu Leu Ala Gly Ala Ala Ala Leu Ala Ser Gly Ser Gln
            20                  25                  30

Gly Asp Arg Glu Pro Val Tyr Arg Asp Cys Val Leu Gln Cys Glu Glu
        35                  40                  45

Gln Asn Cys Ser Gly Gly Ala Leu Asn His Phe Arg Ser Arg Gln Pro
    50                  55                  60

Ile Tyr Met Ser Leu Ala Gly Trp Thr Cys Arg Asp Asp Cys Lys Tyr
65                  70                  75                  80
```

```
Glu Cys Met Trp Val Thr Val Gly Leu Tyr Leu Gln Glu Gly His Lys
                 85                  90                  95

Val Pro Gln Phe His Gly Lys Trp Pro Phe Ser Arg Phe Leu Phe Phe
            100                 105                 110

Gln Glu Pro Ala Ser Ala Val Ala Ser Phe Leu Asn Gly Leu Ala Ser
        115                 120                 125

Leu Val Met Leu Cys Arg Tyr Arg Thr Phe Val Pro Ala Ser Ser Pro
    130                 135                 140

Met Tyr His Thr Cys Val Ala Phe Ala Trp Val Ser Leu Asn Ala Trp
145                 150                 155                 160

Phe Trp Ser Thr Val Phe His Thr Arg Asp Thr Asp Leu Thr Glu Lys
                165                 170                 175

Met Asp Tyr Phe Cys Ala Ser Thr Val Ile Leu His Ser Ile Tyr Leu
            180                 185                 190

Cys Cys Val Arg Thr Val Gly Leu Gln His Pro Ala Val Val Ser Ala
        195                 200                 205

Phe Arg Ala Leu Leu Leu Leu Met Leu Thr Val His Val Ser Tyr Leu
    210                 215                 220

Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn Leu Val Ala Asn Val Ala
225                 230                 235                 240

Ile Gly Leu Val Asn Val Val Trp Trp Leu Ala Trp Cys Leu Trp Asn
                245                 250                 255

Gln Arg Arg Leu Pro His Val Arg Lys Cys Val Val Val Val Leu Leu
            260                 265                 270

Leu Gln Gly Leu Ser Leu Leu Glu Leu Leu Asp Phe Pro Pro Leu Phe
        275                 280                 285

Trp Val Leu Asp Ala His Ala Ile Trp His Ile Ser Thr Ile Pro Val
    290                 295                 300

His Val Leu Phe Phe Ser Phe Leu Glu Asp Asp Ser Leu Tyr Leu Leu
305                 310                 315                 320

Lys Glu Ser Glu Asp Lys Phe Lys Leu Asp
                325                 330
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<210> 18
<211> 1284
<212> DNA
<213> Homo sapiens

<220>
<223> BCN4, ESTs, secreted protein

<220>
<221> CDS
<222> (143)..(874)
<223> BCN4

<400> 18
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cgctgcccgg cagccgggag ccatgcgacc ccagggcccc gccgcctccc cgcagcggct 180
ccgcggcctc ctgctgctcc tgctgctgca gctgcccgcg ccgtcgagcg cctctgagat 240
ccccaagggg aagcaaaagg cgcagctccg gcagagggag gtggtggacc tgtataatgg 300
aatgtgctta caagggccag caggagtgcc tggtcgagac gggagccctg gggccaatgg 360
cattccgggt acacctggga tcccaggtcg ggatggattc aaaggagaaa aggggaatg 420
tctgagggaa agctttgagg agtcctggac acccaactac aagcagtgtt catggagttc 480
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tggttagaat actttcttca tagtcacatt ctctcaacct ataatttgga atattgttgt 1140
ggtcttttgt tttttctctt agtatagcat ttttaaaaaa atataaaagc taccaatctt 1200
tgtacaattt gtaaatgtta agaatttttt ttatatctgt taaataaaaa ttatttccaa 1260
caaccttaaa aaaaaaaaaa aaaa 1284

<210> 19
<211> 243
<212> PRT
<213> Homo sapiens

<220>
<223> BCN4, ESTs, secreted protein

<400> 19
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly Leu
1 5 10 15

Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu
20 25 30

Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu Val Val
35 40 45

Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly
50 55 60

Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly Ile
65 70 75 80

Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu
85 90 95

Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser
100 105 110

Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe
115 120 125

Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly Ser
130 135 140

```
Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr
145                 150                 155                 160

Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile
                165                 170                 175

Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His
            180                 185                 190

Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu
        195                 200                 205

Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly
    210                 215                 220

Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
225                 230                 235                 240

Leu Pro Lys


<210> 20
<211> 243
<212> PRT
<213> Mus sp.

<220>
<223> mouse BCN4, ESTs, mouse orthologue of human BCN4

<220>
<221> MOD_RES
<222> (1)..(243)
<223> Xaa = any amino acid

<400> 20
Xaa Xaa Xaa Xaa Ala Ala Pro Pro Gln Leu Leu Leu Gly Leu Phe Leu
  1               5                  10                  15

Val Leu Leu Leu Leu Leu Gln Leu Ser Ala Pro Ser Ser Ala Ser Glu
             20                  25                  30

Asn Pro Lys Val Lys Gln Lys Ala Leu Ile Arg Gln Arg Glu Val Val
         35                  40                  45

Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly
     50                  55                  60

Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly Ile
 65                  70                  75                  80

Pro Cys Gln Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu
                85                  90                  95

Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser
            100                 105                 110

Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe
        115                 120                 125

Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly Ser
    130                 135                 140
```

Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr
145 150 155 160

Phe Asn Gly Ala Glu Cys Ser Gly Pro Pro Pro Ile Glu Ala Ile Xaa
165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Asp Tyr Pro Lys Gly
210 215 220

Asp Ala Tyr Thr Gly Trp Asp Ser Val Ser Arg Ile Ile Ile Glu Glu
225 230 235 240

Leu Pro Lys